

Software version 4.5
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EM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 08:01:55 : Search time 18:45:05 seconds

(with all comments)
227,352 Million total updates/seq

EM NUCLEIC

Perfect score: 20

Sequence: 1

Scoring table:

Search: 1787656 seqs, 10468268294 residues

Total number of hits satisfying chosen parameters: 524256

Minimum DB seq length: 6

Maximum DB seq length: 50

Post-Processing: Maximum Match 98

List the first 45 summaries

```
Database:
1: qb_kat*
2: qb_kat*
3: qb_kat*
4: qb_kat*
5: qb_kat*
6: qb_kat*
7: qb_kat*
8: qb_kat*
9: qb_kat*
10: qb_kat*
11: qb_kat*
12: qb_kat*
13: qb_kat*
14: qb_kat*
15: qb_kat*
16: qb_kat*
17: qb_kat*
18: qb_kat*
19: qb_kat*
20: qb_kat*
21: qb_kat*
22: qb_kat*
23: qb_kat*
24: qb_kat*
25: qb_kat*
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28: qb_kat*
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30: qb_kat*
31: qb_kat*
32: qb_kat*
33: qb_kat*
34: qb_kat*
35: qb_kat*
36: qb_kat*
37: qb_kat*
38: qb_kat*
39: qb_kat*
40: qb_kat*
41: qb_kat*
42: qb_kat*
43: qb_kat*
44: qb_kat*
45: qb_kat*
```

Foot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit printed and is derived by analysis of the total score distribution.

SUMMARY

Post: 8
Query: 8
Score: 8
Match: 8
Length: 8
ID: 8
Description: 8

1	20	100.0	20	5	AR029127	AR029127	Sequence
2	20	100.0	20	6	AR06511	AR06511	Sequence
3	20	100.0	20	6	AR06602	AR06602	Sequence
4	20	100.0	20	6	AR07662	AR07662	Sequence
5	20	100.0	20	6	AR09634	AR09634	Sequence
6	20	100.0	20	6	AR10272	AR10272	Sequence
7	20	100.0	20	6	AR11067	AR11067	Sequence
8	20	100.0	20	6	AR11764	AR11764	Sequence
9	20	100.0	20	6	AR11764	AR11764	Sequence
10	20	100.0	20	6	AR12105	AR12105	Sequence
11	20	100.0	20	6	AR12105	AR12105	Sequence
12	20	100.0	20	6	AR12443	AR12443	Sequence
13	20	100.0	20	6	AR12443	AR12443	Sequence
14	20	100.0	20	6	AR12508	AR12508	Sequence
15	20	100.0	20	6	AR12657	AR12657	Sequence
16	20	100.0	20	6	AR12937	AR12937	Sequence
17	20	100.0	20	6	AR13008	AR13008	Sequence
18	20	100.0	20	6	AR13075	AR13075	Sequence
19	20	100.0	20	6	AR13406	AR13406	Sequence
20	20	100.0	20	6	AR14247	AR14247	Sequence
21	20	100.0	20	6	AR15014	AR15014	Sequence
22	20	100.0	20	6	AR15702	AR15702	Sequence
23	20	100.0	20	6	AR15784	AR15784	Sequence
24	20	100.0	20	6	AR16070	AR16070	Sequence
25	20	100.0	20	6	AR16079	AR16079	Sequence
26	20	100.0	20	6	AR16241	AR16241	Sequence
27	20	100.0	20	6	AR16247	AR16247	Sequence
28	20	100.0	20	6	AR16374	AR16374	Sequence
29	20	100.0	20	6	AR16383	AR16383	Sequence
30	20	100.0	20	6	AR16417	AR16417	Sequence
31	20	100.0	20	6	AR16417	AR16417	Sequence
32	20	100.0	20	6	AR16419	AR16419	Sequence
33	20	100.0	20	6	AR16540	AR16540	Sequence
34	20	100.0	20	6	AR16540	AR16540	Sequence
35	20	100.0	20	6	AR16540	AR16540	Sequence
36	20	100.0	20	6	AR16548	AR16548	Sequence
37	20	100.0	20	6	AR16548	AR16548	Sequence
38	20	100.0	20	6	AR17267	AR17267	Sequence
39	20	100.0	20	6	AR17267	AR17267	Sequence
40	20	100.0	20	6	AR17441	AR17441	Sequence
41	20	100.0	20	6	AR17441	AR17441	Sequence
42	20	100.0	20	6	AR17441	AR17441	Sequence
43	20	100.0	20	6	AR17441	AR17441	Sequence
44	20	100.0	20	6	AR17441	AR17441	Sequence
45	20	100.0	20	6	AR17441	AR17441	Sequence

REFERENCES

RESUME	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
DEFINITION	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
ACCESSION	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
VERSION	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
KEYWORDS	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
SOURCE	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
ORGANISM	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
REFERENCE	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
AUTHORS	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
TITLE	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
JOURNAL	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
FEATURES	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
BASE COUNT	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence
ORIGIN	1	AR029127	Sequence	1 to 20	Foot. No. 5	AR029127	Sequence

Query Match: 100.0% Score: 500.000
Best Local Similarity: 100.0% Foot. No. 5

[illegible][illegible]



1. *Chlorophyll a* (Chl *a*)

Matches	20; Conservative	20; Moderate	20; Misadventures	20; Indolence	20; Infatuation
1	1	1	1	1	1
2	1	1	1	1	1
3	1	1	1	1	1
4	1	1	1	1	1
5	1	1	1	1	1
6	1	1	1	1	1
7	1	1	1	1	1
8	1	1	1	1	1
9	1	1	1	1	1
10	1	1	1	1	1
11	1	1	1	1	1
12	1	1	1	1	1
13	1	1	1	1	1
14	1	1	1	1	1
15	1	1	1	1	1
16	1	1	1	1	1
17	1	1	1	1	1
18	1	1	1	1	1
19	1	1	1	1	1
20	1	1	1	1	1

2007 March 100.0% Score 20: 18 20: 18 20: 18
 Best Local Similarity: 100.0% Prod. No. 1.3
 Matches 20: Conserved 0: Mismatches 0: Indels 0: Gaps 0

RESULT 13

AAK18711 standard: DNA: 20 bp.

AAK21002 standard: DNA: 20 bp.

AAK21002 standard: DNA: 20 bp.

14-MAY-1999 (first entry)

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14-MAY-1999 (first entry)

14-MAY-1999 (first entry)

14-MAY-1999 (first entry)



PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 207,704
 FILING DATE: 29 AUG 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Joseph Lucet
 REGISTRATION NUMBER: 44,407
 REFERENCE/EXCER NUMBER: 1010 2008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3449
 TELEFAX: 215-568-3449
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MODIFIED BASES: DNA (genomic)
 SEQ ID NO: 10: 10

Query Match: 100.0% Score 209 DB 1 Length 209
 Best Local Similarity: 100.0% Prod. No. 0.44
 Matches: 209 Conserved: 0 Mismatches: 0 Indels: 0 Gaps: 0
 QY 1 Local/Global/Exact 20
 ID 1 Local/Global/Exact 20

RESULT 5
 US-08-203-084-2
 Sequence 2: Application US/seq200004
 Patent No. 5582986
 GENERAL INFORMATION:
 APPLICANT: Modica et al.
 TITLE OF INVENTION: ANTICANCER AND PROSTATE TREATMENT
 FILING DATE: 06 JUN 1996
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Korte
 STREET: One Liberty Place 40th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PC/XT
 OPERATING SYSTEM: PC DOS
 SOFTWARE: WORDPERFECT 5.00
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MODIFIED BASES: DNA (genomic)
 SEQ ID NO: 10: 10
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MODIFIED BASES: DNA (genomic)
 SEQ ID NO: 10: 10

ANTI SENSE: YES
 US-08-203-084-2

Query Match: 100.0% Score 209 DB 1 Length 209
 Best Local Similarity: 100.0% Prod. No. 0.44
 Matches: 209 Conserved: 0 Mismatches: 0 Indels: 0 Gaps: 0

QY 1 Local/Global/Exact 20
 ID 1 Local/Global/Exact 20

RESULT 4
 US-08-469-851A-10
 Sequence 10: Application US/seq4697027A
 Patent No. 5607928
 GENERAL INFORMATION:
 APPLICANT: Cook and Bako
 TITLE OF INVENTION: CELL PROLIFERATION INHIBITING PROSTAGLANDIN
 FILING DATE: 06 JUN 1996
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Korte
 STREET: One Liberty Place 40th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: U.S.A.
 ZIP: 19104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch disk, 720 KB
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: WordPerfect 5.1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MODIFIED BASES: DNA (genomic)
 SEQ ID NO: 10: 10
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: 5' to 3'
 MODIFIED BASES: DNA (genomic)
 SEQ ID NO: 10: 10

Query Match: 100.0% Score 209 DB 1 Length 209
 Best Local Similarity: 100.0% Prod. No. 0.44
 Matches: 209 Conserved: 0 Mismatches: 0 Indels: 0 Gaps: 0
 QY 1 Local/Global/Exact 20
 ID 1 Local/Global/Exact 20

RESULT 7
 US-08-469-851A-10
 Sequence 10: Application US/seq4697027A
 Patent No. 5607928
 GENERAL INFORMATION:
 APPLICANT: Cook and Bako

1 CALLING PARTY: 11 SEP 1946
 2 CLASSIFICATION: 514
 3 PRIOR APPLICATION DATA:
 4 APPLICATION NUMBER: 642312 948
 5 FILING DATE: 25 MAR 1944
 6 ALTERNATIVE INFORMATION:
 7 NAME: JANE MESSY LITATA
 8 DISTRIBUTION NUMBER: 42,257
 9 ADDRESS: 2500 EIGHT HARBOR, NEW ORLEANS,
 10 TELEPHONE: (609) 779-2400
 11 TELETYPE: (609) 779-9433
 12 INFORMATION FOR STUDY NO. 4:
 13 SEQUENCE CHARACTERISTICS:
 14 LENGTH: 20
 15 TYPE: Nucleic Acid
 16 STRANDNESS: Single
 17 TOPLOGY: Linear
 18 ANALYSIS: Yes
 19 IN 08 712-145-4



Class: plasmid ends
High quality sequence steps: 19.
Location/Qualifiers

FEATURES

1..19

Source "Mus musculus"

Accession "U00001"

Version "1.0"

Keywords "mus musculus"

Organism "Mus musculus"

Strain "Mus musculus"

Sex "Male"

Age "Adult"

Sex "Male"

Age "Adult"

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Sex "Male"

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Sex "Male"

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Sex "Male"

Age "Adult"

Seq primer: CTGTCGAAAGTAAAGGAGTAA
Class: plasmid ends
High quality sequence steps: 22.
Location/Qualifiers

FEATURES

1..22

Source "Mus musculus"

Accession "U00001"

Version "1.0"

Keywords "mus musculus"

Organism "Mus musculus"

Strain "Mus musculus"

Sex "Male"

Age "Adult"

Sex "Male"

Age "Adult"

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